

Exhibit I


Query: SEQ ID NO: 7

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (17 letters)

Results for: lcl|11866 None(17bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|11866

Description

None

Molecule type

nucleic acid

Query Length

17

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Distance tree of results](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 28, 2008 5:47 PM
Number of letters	252,991,180
Number of sequences	7,851,115
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	15
Effective length of query	2
Effective length of database	25605224455
Effective search space	51210448910
Effective search space used	51210448910

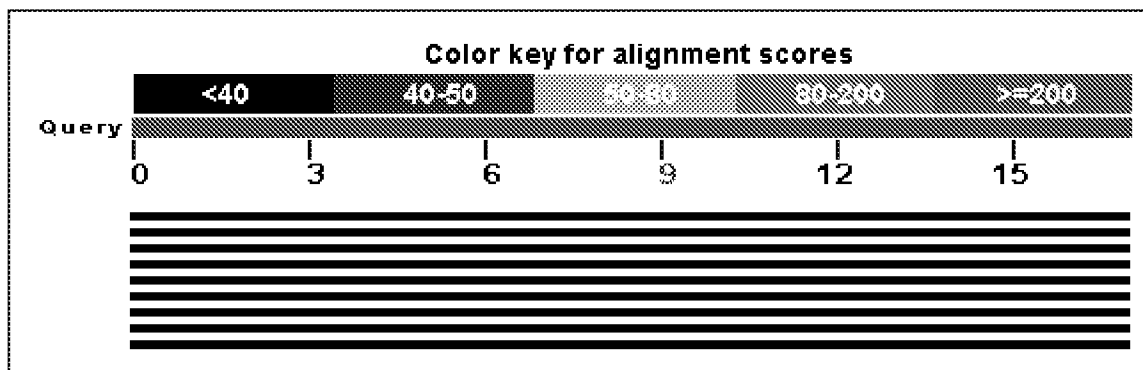
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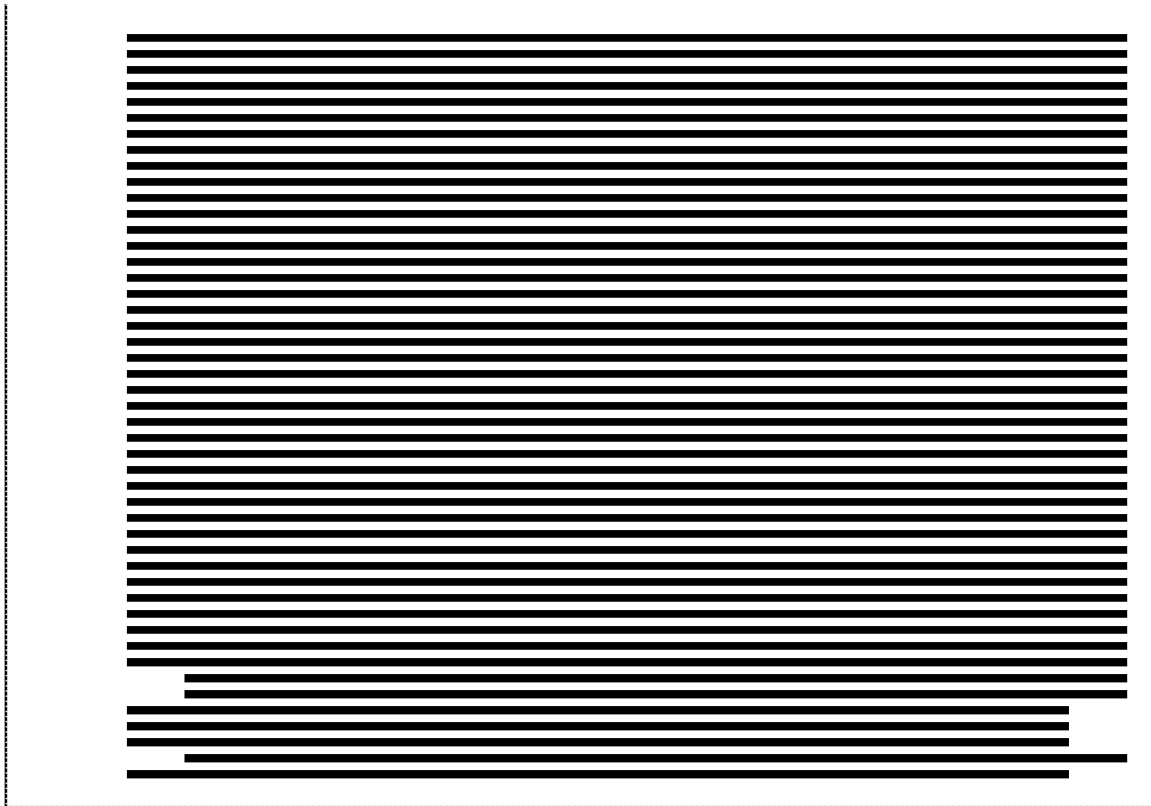
Graphic Summary

Distribution of 129 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.








Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)



NW_002196569.1	Ralstonia solanacearum IPO1609 >emb CU914168.1 Ralstonia solanacearum strain IPO1609 Genome Draft	34.2	34.2	100%	2.6	100%	
NW_002196522.1	Ralstonia solanacearum MolK2 >emb CU694390.1 Ralstonia solanacearum strain MolK2 Genome Draft	34.2	34.2	100%	2.6	100%	
XM_001915641.1	PREDICTED: Equus caballus similar to Glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase- gastrointestinal) (GSHPx-GI) (LOC100146145), mRNA	34.2	34.2	100%	2.6	100%	
XM_001916096.1	PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA	34.2	34.2	100%	2.6	100%	
CP000958.1	Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence	34.2	112	100%	2.6	100%	
NM_001115119.1	Canis lupus familiaris glutathione peroxidase 1 (GPX1), mRNA	34.2	34.2	100%	2.6	100%	 
XR_038530.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2	34.2	100%	2.6	100%	
XR_038228.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2	34.2	100%	2.6	100%	
NM_001077512.2	Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA	34.2	34.2	100%	2.6	100%	
CP000458.1	Burkholderia cenocepacia HI2424 chromosome 1, complete sequence	34.2	112	100%	2.6	100%	
AK239914.1	Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus	34.2	34.2	100%	2.6	100%	
AK231261.1	Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine	34.2	34.2	100%	2.6	100%	
AB121000.1	Callithrix jacchus gp1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%	
AB120996.1	Pan troglodytes gp1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%	
CT573213.2	Frankia alni str. ACN14A chromosome, complete sequence	34.2	86.7	100%	2.6	100%	
AK225835.1	Homo sapiens mRNA for Glutathione peroxidase 1 variant, clone: FCC127C01	34.2	34.2	100%	2.6	100%	 
XR_013650.1	PREDICTED: Macaca mulatta similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA	34.2	34.2	100%	2.6	100%	 
CP000380.1	Burkholderia cenocepacia AU 1054 chromosome 3, complete sequence	34.2	34.2	100%	2.6	100%	
AY966403.1	Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA, complete cds	34.2	34.2	100%	2.6	100%	
CP000151.1	Burkholderia sp. 383 chromosome 1, complete sequence	34.2	60.5	100%	2.6	100%	
BC007865.2	Homo sapiens glutathione peroxidase 1,	34.2	34.2	100%	2.6	100%	 

	mRNA (cDNA clone MGC:14399 IMAGE:4301275), complete cds									
BC000742.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:2335 IMAGE:3505654), complete cds	34.2	34.2	100%	2.6	100%	UE G			
BC070258.1	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:88245 IMAGE:6452792), complete cds	34.2	34.2	100%	2.6	100%	UE G			
AY572225.1	Canis familiaris glutathione peroxidase 1 mRNA, partial cds	34.2	34.2	100%	2.6	100%	UG			
AC135371.2	Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	34.2	34.2	100%	2.6	100%				
AY327818.1	Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cds	34.2	34.2	100%	2.6	100%	G			
NM_214201.1	Sus scrofa glutathione peroxidase 1 (GPX1), mRNA >gb AF532927.1 Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, complete cds	34.2	34.2	100%	2.6	100%	UG			
AB120999.1	Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%				
AB120998.1	Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%				
AB120997.1	Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%				
DQ333996.1	Spermophilus parryii clone SP00035 glutathione peroxidase 1 mRNA, partial cds	34.2	34.2	100%	2.6	100%				
M83094.1	Homo sapiens cytosolic selenium- dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end	34.2	34.2	100%	2.6	100%	EG			
Y00483.1	Human gene for glutathione peroxidase	34.2	34.2	100%	2.6	100%	EG			
Y00433.1	Human mRNA for glutathione peroxidase (EC 1.11.1.9.)	34.2	34.2	100%	2.6	100%	UE G			
X13710.1	H.sapiens unspliced mRNA for glutathione peroxidase	34.2	34.2	100%	2.6	100%	UE G			
X13709.1	Human gpx1 mRNA for glutathione peroxidase	34.2	34.2	100%	2.6	100%	UG			
NM_001085444.1	Oryctolagus cuniculus glutathione peroxidase 1 (GPX1), mRNA >emb X13837.1 OCGPO Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)	34.2	34.2	100%	2.6	100%	UG			
M21304.1	Human glutathione peroxidase (GPX1) mRNA, complete cds	34.2	34.2	100%	2.6	100%	UE G			
U39842.1	Cavia porcellus glutathione peroxidase mRNA, partial cds	34.2	34.2	100%	2.6	100%				
CR626479.1	full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapiens (human)	34.2	34.2	100%	2.6	100%	UG			
CR620255.1	full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%	UG			
CR614747.1	full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%	UG			
CR601795.1	full-length cDNA clone CS0DI068YJ17 of	34.2	34.2	100%	2.6	100%	UG			

12/29/08

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[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|NW_002196569.1|  *Ralstonia solanacearum* IPO1609
 emb|CU914168.1|  *Ralstonia solanacearum* strain IPO1609 Genome Draft
 Length=3372855

Features in this part of subject sequence:
 glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus


```
Query 1          CTCGGCTTCCCGTGCAA 17
                |||||
Sbjct 2635709    CTCGGCTTCCCGTGCAA 2635693
```

>ref|NW_002196522.1|  *Ralstonia solanacearum* MolK2
 emb|CU694390.1|  *Ralstonia solanacearum* strain MolK2 Genome Draft
 Length=237010

Features in this part of subject sequence:
 glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus


```
Query 1          CTCGGCTTCCCGTGCAA 17
                |||||
Sbjct 131900     CTCGGCTTCCCGTGCAA 131916
```

>ref|XM_001915641.1|  PREDICTED: *Equus caballus* similar to Glutathione peroxidase (GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) (LOC100146145), mRNA
 Length=573

GENE ID: 100146145 LOC100146145 | similar to Glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) [*Equus caballus*]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

```
Query 1          CTCGGCTTCCCGTGCAA 17
                |||||
Sbjct 190        CTCGGCTTCCCGTGCAA 206
```


>ref|XM_001916096.1|  PREDICTED: *Equus caballus* similar to glutathione peroxidase (LOC100053396), mRNA

Length=606

GENE ID: 100053396 LOC100053396 | similar to glutathione peroxidase 1 [Equus caballus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 214    CTCGGCTTCCCGTGCAA 230
```

>gb|CP000958.1|  Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence
Length=3532883

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 2284247 CTCGGCTTCCCGTGCAA 2284231
```

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 3      CGGCTTCCCGTGC 15
           |||||
Sbjct 2569429 CGGCTTCCCGTGC 2569417
```

Features in this part of subject sequence:
conserved hypothetical protein


Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 2872181 CTCGGCTTCGCGTGCAA 2872165
```

Features in this part of subject sequence:
diguanylate cyclase

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus


```
Query 3      CGGCTTCCCGTGC 15
           |||||
Sbjct 3526443 CGGCTTCCCGTGC 3526455
```

>ref|NM_001115119.1|  Canis lupus familiaris glutathione peroxidase 1 (GPX1)
Length=838

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 235    CTCGGCTTCCCGTGCAA 251
```

>ref|XR_038530.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
 Length=876

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1)
 (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 253    CTCGGCTTCCCGTGCAA 269
```

>ref|XR_038228.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
 Length=878

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1)
 (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 255    CTCGGCTTCCCGTGCAA 271
```

>ref|NM_001077512.2|  Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA
 Length=613

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
 (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 221    CTCGGCTTCCCGTGCAA 237
```

>gb|CP000458.1|  Burkholderia cenocepacia HI2424 chromosome 1, complete sequence
 Length=3483902

Sort alignments for this
 E value Score Percent
 Query start position

Features in this part of subject sequence:
 Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 2258895 CTCGGCTTCCCGTGCAA 2258879
```

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query   3           CGGCTTCCCGTGC   15
          |||||
Sbjct  2528844 CGGCTTCCCGTGC   2528832
```

Features in this part of subject sequence:
conserved hypothetical protein


Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```
Query   1           CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  2825631 CTCGGCTTCGCGTGCAA   2825615
```

Features in this part of subject sequence:
conserved hypothetical protein


Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query   1           CTCGGCTTCCCGT   13
          |||||
Sbjct  3438094 CTCGGCTTCCCGT   3438082
```

>dbj|AK239914.1|  Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus
Length=912

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query   1           CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  312   CTCGGCTTCCCGTGCAA   328
```

>dbj|AK231261.1|  Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine
Length=936


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query   1           CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  327   CTCGGCTTCCCGTGCAA   343
```

>dbj|AB121000.1| Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, comp
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query   1           CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  214   CTCGGCTTCCCGTGCAA   230
```

>dbj|AB120996.1|  Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, compl
cds
Length=606

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct  214    CTCGGCTTCCCGTGCAA 230
```

>emb|CT573213.2|  Frankia alni str. ACN14A chromosome, complete sequence
Length=7497934

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct  1918274 CTCGGCTTCCCGTGCAA 1918290
```

Features flanking this part of subject sequence:
93 bp at 5' side: Putative MarR-family transcriptional regulator
53 bp at 3' side: Putative transcriptional regulator


Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

```
Query 4      GGCTTCCCGTGCA 16
            |||||
Sbjct  641315  GGCTTCCCGTGCA 641327
```

Features in this part of subject sequence:
hypothetical protein; putative Amidohydrolase domain

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

```
Query 3      CGGCTTCCCGTGC 15
            |||||
Sbjct  1575841 CGGCTTCCCGTGC 1575853
```


>dbj|AK225835.1|  Homo sapiens mRNA for Glutathione peroxidase 1 variant, clo
FCC127C01
Length=874

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
```


Sbjct 223 CTCGGCTTCCCGTGCAA 239

>ref|XR_013650.1|  PREDICTED: Macaca mulatta similar to Glutathione peroxidase (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA
Length=811

GENE ID: 706732 LOC706732 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Macaca mulatta]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 205 CTCGGCTTCCCGTGCAA 221

>gb|CP000380.1|  Burkholderia cenocepacia AU 1054 chromosome 3, complete sequence
Length=1196094

Features in this part of subject sequence:
Glutathione peroxidase


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 632809 CTCGGCTTCCCGTGCAA 632825

>gb|AY966403.1| Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA complete cds
Length=858

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 237 CTCGGCTTCCCGTGCAA 253

>gb|CP000151.1|  Burkholderia sp. 383 chromosome 1, complete sequence
Length=3694126

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 2403347 CTCGGCTTCCCGTGCAA 2403331


Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```

Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 3002445 CTCGGCTTCGCGTGCAA 3002429

```

>gb|BC007865.2|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC: IMAGE:4301275), complete cds
Length=851


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 230    CTCGGCTTCCCGTGCAA 246

```

>gb|BC000742.2|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:3505654), complete cds
Length=863


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 243    CTCGGCTTCCCGTGCAA 259

```

>gb|BC070258.1|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:6452792), complete cds
Length=866


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 236    CTCGGCTTCCCGTGCAA 252

```

>gb|AY572225.1|  Canis familiaris glutathione peroxidase 1 mRNA, partial cds
Length=434


GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```


Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 175    CTCGGCTTCCCGTGCAA 191

```

>gb|AC135371.2|  Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=25901

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus



```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 8993    CTCGGCTTCCCGTGCAA 8977
```

>gb|AY327818.1|  Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cd
Length=4877

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 2385    CTCGGCTTCCCGTGCAA 2401
```

>ref|NM_214201.1|  Sus scrofa glutathione peroxidase 1 (GPX1), mRNA
gb|AF532927.1|  Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, com
cds
Length=803

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 235     CTCGGCTTCCCGTGCAA 251
```

>dbj|AB120999.1| Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 214     CTCGGCTTCCCGTGCAA 230
```

>dbj|AB120998.1| Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
          |||||
Sbjct 214     CTCGGCTTCCCGTGCAA 230
```

>dbj|AB120997.1| Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)


Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 214    CTCGGCTTCCCGTGCAA 230
```

>gb|DQ333996.1| *Spermophilus parryii* clone SP00035 glutathione peroxidase 1 mRNA
partial cds
Length=210


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 65     CTCGGCTTCCCGTGCAA 81
```

>gb|M83094.1|HUMGLPEX  *Homo sapiens* cytosolic selenium-dependent glutathione gene, complete cds, and rhoh12 gene, 3' end
Length=4407

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 2774   CTCGGCTTCCCGTGCAA 2790
```

>emb|Y00483.1|HSGSHPXG  Human gene for glutathione peroxidase
Length=1733

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [*Homo sapiens*]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 687    CTCGGCTTCCCGTGCAA 703
```

>emb|Y00433.1|HSGSHPX  Human mRNA for glutathione peroxidase (EC 1.11.1.9.)
Length=1134

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [*Homo sapiens*]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 532    CTCGGCTTCCCGTGCAA 548
```

>emb|X13710.1|HSPEROXP  *H.sapiens* unspliced mRNA for glutathione peroxidase
Length=1100


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [*Homo sapiens*]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query   1      CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  219    CTCGGCTTCCCGTGCAA   235

```

>emb|X13709.1|HSPEROXR  Human gpx1 mRNA for glutathione peroxidase
Length=819



GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query   1      CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  219    CTCGGCTTCCCGTGCAA   235

```

>ref|NM_001085444.1|  Oryctolagus cuniculus glutathione peroxidase 1 (GPX1),
emb|X13837.1|OCGPO  Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)
Length=760


GENE ID: 100009258 GPX1 | glutathione peroxidase 1 [Oryctolagus cuniculus]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query   1      CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  229    CTCGGCTTCCCGTGCAA   245

```

>gb|M21304.1|HUMGLP  Human glutathione peroxidase (GPX1) mRNA, complete cds
Length=856

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query   1      CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  255    CTCGGCTTCCCGTGCAA   271

```


>gb|U39842.1|CPU39842 Cavia porcellus glutathione peroxidase mRNA, partial cds
Length=331

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query   1      CTCGGCTTCCCGTGCAA   17
          |||||
Sbjct  112    CTCGGCTTCCCGTGCAA   128

```


>emb|CR626479.1|  full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapi
(human)
Length=838

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)

Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 234    CTCGGCTTCCCGTGCAA 250
```

>emb|CR620255.1|  full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50 of Homo sapiens (human)
Length=828

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 243    CTCGGCTTCCCGTGCAA 259
```

>emb|CR614747.1|  full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-norm of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 268    CTCGGCTTCCCGTGCAA 284
```

>emb|CR601795.1|  full-length cDNA clone CS0DI068YJ17 of Placenta Cot 25-norm of Homo sapiens (human)
Length=792

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 188    CTCGGCTTCCCGTGCAA 204
```

>emb|CR595371.1|  full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25 of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||||
Sbjct 245    CTCGGCTTCCCGTGCAA 261
```


>dbj|AK130160.1|  Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly simi

to Glutathione peroxidase (EC 1.11.1.9)
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 261    CTCGGCTTCCCGTGCAA 277
```

>gb|AC121247.2|  Homo sapiens chromosome 3 clone RP11-3B7, complete sequence
Length=170787


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 22842   CTCGGCTTCCCGTGCAA 22858
```

>dbj|AB105162.1| Macaca fuscata mRNA for cytosolic glutathione peroxidase, compl
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 214     CTCGGCTTCCCGTGCAA 230
```

>ref|NM_000581.2|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
1, mRNA
Length=921

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 300     CTCGGCTTCCCGTGCAA 316
```

>ref|NM_201397.1|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
2, mRNA
Length=1200

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||||
Sbjct 300     CTCGGCTTCCCGTGCAA 316
```

>gb|CP001111.1|  Stenotrophomonas maltophilia R551-3, complete genome